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What is claimed:

- 1. A method for increasing metabolic flux through the pentose phosphate pathway in a microorganism comprising culturing a microorganism comprising a gene which is deregulated under conditions such that metabolic flux through the pentose phosphate pathway is increased.
- 2. The method of claim 1, wherein fructose or sucrose is used as a carbon source.
 - 3. The method of claim 1, wherein fructose is used as a carbon source.
 - 4. The method of claim 1, wherein the gene is glycerol kinase.
- 15 5. The method of claim 4, wherein the glycerol kinase gene is derived from *Corynebacterium*.
 - 6. The method of claim 4, wherein the glycerol kinase gene is underexpressed.
- 20 7. The method of claim 1, wherein the gene encodes glycerol kinase.
 - 8. The method of claim 7, wherein glycerol kinase has decreased activity.
- 9. The method of claim 1, wherein the microorganism is a Gram positive 25 microorganism.
 - 10. The method of claim 1, wherein the microorganism belongs to the genus Corynebacterium.
- 30 11. The method of claim 10, wherein the microorganism is *Corynebacterium glutamicum*.
 - 12. The method of claim 1, wherein the microorganism is fermented to produce a fine chemical.
 - 13. The method of claim 1, wherein the microorganism further comprises one or more additional deregulated gene.

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14. The method of claim 13, wherein the one or more additional deregulated gene is selected from the group consisting of an ask gene, a dapA gene, an asd gene, a dapB gene, a ddh gene, a lysA gene, a lysE gene, a pycA gene, a zwf gene, a pepCL gene, a gap gene, a zwa1 gene, a tkt gene, a tad gene, a mqo gene, a tpi gene, a pgk gene, and a sigC gene.

- 15. The method of claim 14, wherein the one or more additional deregulated gene is overexpressed.
- 16. The method of claim 13, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a feed-back resistant aspartokinase, a dihydrodipicolinate synthase, an aspartate semialdehyde dehydrogenase, a dihydrodipicolinate reductase, a diaminopimelate dehydrogenase, a diaminopimelate epimerase, a lysine exporter, a pyruvate carboxylase, a glucose-6-phosphate dehydrogenase, a phosphoenolpyruvate carboxylase, a glyceraldedyde-3-phosphate dehydrogenase, an RPF protein precursor, a transketolase, a transaldolase, a menaquinine oxidoreductase, a triosephosphate isomerase, a 3-phosphoglycerate kinase, and an RNA-polymerase sigma factor sigC.
- 20 17. The method of claim 16, wherein the protein has increased activity.

- 18. The method of claim 13, wherein the one or more additional deregulated gene is selected from the group consisting of a pepCK gene, a mal E gene, a glgA gene, a pgi gene, a dead gene, a menE gene, a citE gene, a mikE17 gene, a poxB gene, a zwa2 gene, and a sucC gene.
- 19. The method of claim 18, wherein the one or more additional deregulated gene is attenuated, decreased or repressed.
- 30 20. The method of claim 13, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a phosphoenolpyruvate carboxykinase, a malic enzyme, a glycogen synthase, a glucose-6-phosphate isomerase, an ATP dependent RNA helicase, an o-succinylbenzoic acid-CoA ligase, a citrate lyase beta chain, a transcriptional regulator, a pyruvate dehydrogenase, an RPF protein precursor, and a Succinyl-CoA-Synthetase.
 - 21. The method of claim 20, wherein the protein has decreased activity.

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- 22. A method for producing a fine chemical comprising:
 - a) culturing a microorganism in which glycerol kinase is deregulated; and
 - b) accumulating the fine chemical in the medium or in the cells of the microorganisms, thereby producing a fine chemical.

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- 23. A method for producing a fine chemical comprising culturing a microorganism in which at least one pentose phosphosphate biosynthetic pathway gene or enzyme is deregulated under conditions such that the fine chemical is produced.
- 10 24. The method of claim 23, wherein said biosynthetic gene is glycerol kinase.
 - 25. The method of claim 23, wherein said biosynthetic enzyme is glycerol kinase.
 - 26. The method of claim 22 or 24, wherein glycerol kinase expression is decreased.
 - 27. The method of claim 22 or 25, wherein glycerol kinase activity is decreased.
 - 28. The method of claim 22, further comprising recovering the fine chemical.
- 20 29. The method of claim 22 or 23, wherein one or more additional gene is deregulated.
- 30. The method of claim 29, wherein the one or more additional deregulated gene is selected from the group consisting of an ask gene, a dapA gene, an asd gene, a dapB gene, a ddh gene, a lysA gene, a lysE gene, a pycA gene, a zwf gene, a pepCL gene, a gap gene, a zwal gene, a tkt gene, a tad gene, a mqo gene, a tpi gene, a pgk gene, and a sigC gene.
- 31. The method of claim 30, wherein the one or more additional deregulated gene is overexpressed.
 - 32. The method of claim 29, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a feed-back resistant aspartokinase, a dihydrodipicolinate synthase, an aspartate semialdehyde
- dehydrogenase, a dihydrodipicolinate reductase, a diaminopimelate dehydrogenase, a diaminopimelate epimerase, a lysine exporter, a pyruvate carboxylase, a glucose-6-phosphate dehydrogenase, a phosphoenolpyruvate carboxylase, a glyceraldedyde-3-phosphate dehydrogenase, an RPF protein precursor, a transketolase, a transaldolase, a

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menaquinine oxidoreductase, a triosephosphate isomerase, a 3-phosphoglycerate kinase, and an RNA-polymerase sigma factor sigC.

33. The method of claim 32, wherein the protein has increased activity.

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34. The method of claim 29, wherein the one or more additional deregulated gene is selected from the group consisting of a pepCK gene, a mal E gene, a glgA gene, a pgi gene, a dead gene, a menE gene, a citE gene, a mikE17 gene, a poxB gene, a zwa2 gene, and a sucC gene.

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- 35. The method of claim 34, wherein the one or more additional deregulated gene is attenuated, decreased or repressed.
- 36. The method of claim 29, wherein the one or more additional deregulated gene encodes a protein selected from the group consisting of a phosphoenolpyruvate carboxykinase, a malic enzyme, a glycogen synthase, a glucose-6-phosphate isomerase, an ATP dependent RNA helicase, an o-succinylbenzoic acid-CoA ligase, a citrate lyase beta chain, a transcriptional regulator, a pyruvate dehydrogenase, an RPF protein precursor, and a Succinyl-CoA-Synthetase.

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- 37. The method of claim 36, wherein the protein has decreased activity.
- 38. The method of claim 22 or 23, wherein the microorganism is a Gram positive microorganism.

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- 39. The method of claim 22 or 23, wherein the microorganism belongs to the genus *Corynebacterium*.
- 40. The method of claim 39, wherein the microorganism is *Corynebacterium* 30 glutamicum.
 - 41. The method of claim 22 or 23, wherein the fine chemical is lysine.
 - 42. The method of claim 41, wherein lysine is produced at a yield of at least 100 g/L.
 - 43. The method of claim 41, wherein lysine is produced at a yield of at least 150 g/L.

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44. The method of claim 22 or 23, wherein fructose or sucrose is used as a carbon source.

45. The method of claim 22 or 23, wherein fructose is used as a carbon source.

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- 46. The method of claim 22 or 24, wherein glycerol kinase comprises the nucleotide sequence of SEQ ID NO:1.
- 47. The method of claim 22 or 24, wherein glycerol kinase encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.
 - 48. A recombinant microorganism which has a deregulated pentose phosphate biosynthesis pathway.
- 15 49. A recombinant microorganism comprising a deregulated pentose phosphate biosynthesis gene.
 - 50. The recombinant microorganism of claim 49, wherein said deregulated gene is glycerol kinase.

- 51. The recombinant microorganism of claim 50, wherein glycerol kinase expression is decreased.
- 52. The recombinant microorganism of claim 50, wherein said glycerol kinase gene encodes a glycerol kinase protein having decreased activity.
 - 53. The recombinant microorganism of claim 49, wherein the microorganism belongs to the genus *Corynebacterium*.
- The recombinant microorganism of claim 53, wherein the microorganism is Corynebacterium glutamicum.